

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 28, 2003, 09:51:49 ; Search time 2055 Seconds
(without alignments)
1596.644 Million cell updates/sec

Title: US-09-866-582A-2
Perfect score: 661
Sequence: 1 MDVAVRGVYDEDFHVRILD.....GEOELMIQKLSRSSGAAYV 135

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5
Ygapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=EST -QFWT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09866582@cgn.1.1.2874.@runat_27082003_095333_9839 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estm:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	577	87.3	466	9	AV392837	AV392837 AV392837
2	227	34.3	493	10	BE352290	BE352290 894059C02
3	202	30.6	646	13	BW280429	BW280429 BW280429
4	202	30.6	653	13	BW280674	BW280674 BW280674
5	200	30.3	540	12	BP026060	BP026060 BP026060
6	200	30.3	541	9	AY964246	AY964246 AV964246
7	200	30.3	565	13	BW215694	BW215694 BW215694
8	200	30.3	576	12	BP013658	BP013658 BP013658
9	200	30.3	670	12	BP008971	BP008971 BP008971
10	200	30.3	680	13	BW298785	BW298785 BW298785
11	200	30.3	683	13	BW313621	BW313621 BW313621
12	200	30.3	715	13	BW079944	BW079944 BW079944
13	200	30.3	719	13	BW168960	BW168960 BW168960
14	200	30.3	720	13	BW077451	BW077451 BW077451
15	200	30.3	755	13	BW213159	BW213159 BW213159
16	200	30.3	758	9	AV897763	AV897763 AV897763
17	200	30.3	759	13	BW312507	BW312507 BW312507
18	198	30.0	615	13	BQ393735	BQ393735 NISC_0905
19	198	30.0	619	9	AL791937	AL791937 AL791937
20	198	30.0	629	9	AL649467	AL649467 AL649467
21	198	30.0	640	9	AL637277	AL637277 AL637277
22	197	29.9	418	13	BY635126	BY635126 BY635126
23	197	29.8	715	13	BW150890	BW150890 BW150890
24	196	29.7	633	13	BW286181	BW286181 BW286181
25	196	29.7	661	9	AV899426	AV899426 AV899426
26	196	29.7	674	13	BW248613	BW248613 BW248613
27	196	29.7	718	13	BW156639	BW156639 BW156639
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37	194.5	29.4	454	10	BE132868	BE132868 uf37b12.x
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41	194.5	29.4	517	13	BQ208726	BQ208726 UI-R-DY1-
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45	194.5	29.4	633	14	CA977210	CA977210 AGENCOURT
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53	194	29.3	391	10	BE626846	BE626846 ut88d02.x
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56	194	29.3	464	13	EX274751	EX274751 BX274751
57	194	29.3	553	12	BM894690	BM894690 ih70c01.y
58	194	29.3	614	10	BG711517	BG711517 pg11n.pk0
59	194	29.3	614	13	B0347180	B0347180 60417259
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79 194 29.3 922 13 BU458001
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82 192.5 29.1 428 10 BU789469
83 192 29.0 391 10 BF075390
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85 192 29.0 457 9 AA099304
86 192 29.0 461 9 AA273692
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88 192 29.0 553 10 BF075374
89 192 29.0 611 12 BF1713151
90 192 29.0 626 13 BQ632674
91 192 29.0 750 13 BX099677
92 192 29.0 876 13 BX413118
93 192 29.0 922 13 BU914040
94 191 28.9 495 14 N40217
95 191 28.9 510 13 BU074070
96 191 28.9 513 12 BU029640
97 191 28.9 531 10 BF075368
98 191 28.9 647 14 CA381325
99 191 28.9 649 13 BU077234
100 191 28.9 1050 13 BX419276

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ALIGNMENTS

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RESULT 1
AV392837 466 bp mRNA linear EST 23-APR-2002
LOCUS AV392837 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
DEFINITION AV392837 cDNA clone CM100a09_r 5', mRNA sequence.
ACCESSION AV392837.1 GI:6547053
VERSION AV392837.1
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeaceae; Chlamydomonas.

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REFERENCE
AUTHORS Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
PUBMED 10691129
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..466
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"

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FEATURES
source

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/clone="CM100a09_r"
/dev_stage="photoautotrophic growth"
/clone_lib="Chlamydomonas reinhardtii C9"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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Alignment Scores:
Pred. No.: 1..15e-40 Length: 466
Score: 577.00 Matches: 122
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 99.19% Mismatches: 1
Query Match: 87.29% Indels: 1
DB: 9 Gaps: 0
US-09-866-582a-2 (1-135) x AV392837 (1-466)
QY 1 MetAspAlaValAspArgGlyValtyrPheAspGluAspPheHisValArgIleLeuAsp 20
Db 98 ATGACGCGGTAGATAGAGGAGTCTACTTTGACGAGGACTTTCATGTCGCCGATCTTGAT 157
QY 21 ValAspLysTyrAsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsn 40
Db 158 GTTGACAAAGTACAAATGCTTCAAGTCGCTCCAGGACACACAAATGTTTCATTAAACAAC 217
QY 41 IleGlnAsnMetGlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGlu 60
Db 218 ATCCAAATATGCAAGCGCTCGTGGACAAGTACGTCGCCCATCGCAGCAGGCTCGAG 277
QY 61 ArgLeuGluAlaGluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaLeuSer 80
Db 278 CGGCTAGAAGCTGAAAAGCTGAGGCCATTTGGCTCGGGAACCGGTTGGCTCGCTGAGC 337
QY 81 GluGluArgLysArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGlu 100
Db 338 GAGGAGCGGAACGCTAAACAAAGACGAGGAGGCGCATGCTAGCGGAGAGGAGGAGGAG 397
QY 101 LeuGluArgLeuGlnMetGluGlnSerLeuIleLysValLysGlyGluGlnGluLeu 120
Db 398 CTTGAGAGGCTCCAAATGGAGGACGTCGCTGATCAG-GTGAAGGCGGAGGAGGAGCTC 456
QY 121 MetIleGln 123
Db 457 ATGATTCAG 465

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RESULT 2

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LOCUS BE352290 493 bp mRNA linear EST 18-JUL-2000
DEFINITION 894059C02.xl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE352290
VERSION BE352290.1 GI:9264143
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeaceae; Chlamydomonas.
REFERENCE
AUTHORS Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers

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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/notes="vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      88 a 182 c 101 g 122 t
ORIGIN
Alignment Scores:
Pred. No.:      1.76e-10      Length:      493
Score:          227.00      Matches:      48
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    34.34%      Indels:      0
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Qy      108 GluGlnSerLeuLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSerAsp 127
Db      433 GAGCAGTGCCTGATCAAGGTGAAGGGGAGCAGGAGGCTCATGATTCAGAGCTGCGGAC 374
Qy      128 SerSerSerGlyAlaAlaTyrVal 135
Db      373 ACCAGCAGCGGGCGGCATACGTG 350

RESULT 3
BW280429      646 bp      mRNA      linear      EST 11-NOV-2002
LOCUS      BW280429 Nori Satoh unpublished cDNA library, gonad Ciona
DEFINITION      intestinalis cDNA clone cigd013n23 5', mRNA sequence.
ACCESSION      BW280429
VERSION      BW280429.1 GI:24861040
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 646)
AUTHORS      Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-703-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 646
/organism="Ciona intestinalis"
/mol_type="mrna"
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/mol_type="mrna"
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/notes="vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      88 a 182 c 101 g 122 t
ORIGIN
Alignment Scores:
Pred. No.:      1.76e-10      Length:      493
Score:          227.00      Matches:      48
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    34.34%      Indels:      0
DB:             10      Gaps:      0

US-09-866-582a-2 (1-135) x BE352290 (1-493)
Qy      88 LysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMetGlu 107
Db      493 AAGGAGCAGAGCGCCATGCTAGCGGACAGACGAGGAGGCTTGAGAGGCTCCAAATGGAG 434
Qy      108 GluGlnSerLeuLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSerAsp 127
Db      433 GAGCAGTGCCTGATCAAGGTGAAGGGGAGCAGGAGGCTCATGATTCAGAGCTGCGGAC 374
Qy      128 SerSerSerGlyAlaAlaTyrVal 135
Db      373 ACCAGCAGCGGGCGGCATACGTG 350

RESULT 3
BW280429      646 bp      mRNA      linear      EST 11-NOV-2002
LOCUS      BW280429 Nori Satoh unpublished cDNA library, gonad Ciona
DEFINITION      intestinalis cDNA clone cigd013n23 5', mRNA sequence.
ACCESSION      BW280429
VERSION      BW280429.1 GI:24861040
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 646)
AUTHORS      Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-703-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 646
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Score:          202.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:    30.56%      Indels:      0
DB:             13      Gaps:      0

US-09-866-582a-2 (1-135) x BW280429 (1-646)
Qy      7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db      63 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 122
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Qy      47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
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Qy      67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db      243 ATGAAAGCCATCGGTTCTCTGTAAGTCAATTCGCAAGTTCGCAAGCAGAGGAAATCCGAG 302
Qy      87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGlnGluLeuGluArgLeuGlnMet 106
Db      303 CAACAACAGTCAAGGCACTCATAGCGGAGAGAAACACAACTTGACGATTCGATGTG 362
Qy      107 GluGlnSerLeuLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db      363 CAACACCAAGTCTCTAAGAAAACAAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 422
Qy      127 AspSer 128
Db      423 ACTTCT 428

RESULT 4
BW280674      653 bp      mRNA      linear      EST 11-NOV-2002
LOCUS      BW280674 Nori Satoh unpublished cDNA library, gonad Ciona
DEFINITION      intestinalis cDNA clone cigd014j07 5', mRNA sequence.
ACCESSION      BW280674
VERSION      BW280674.1 GI:24861285
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 653)
AUTHORS      Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-703-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 653
/organism="Ciona intestinalis"
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/db_xref="taxon:7719"
/clone="cigd014j07"

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US-09-866-582A-2 (1-135) x BW280674 (1-653)

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Qy	27	SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly	46
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Db	122	ACATCTGACACGAAGAGGAATGCCAGCAATTCGTCGAAATATGCCAGGTTTCAAAA	181
		:	
Qy	47	LeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAlaGluLys	66
		: :	
Db	182	CTTGTTGGTAGCTTCATAGAGATCAGCGAGCCANTGCCAAAAGATGTTGAAATGAGAA	241
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		:	
Db	242	ATGAAGGCATCGGTTCTCGTAACTGCTCAAGTCAATTGCCAAAGCAGAGGAATCCCC	301
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Qy	87	GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet	106
		: : : :	
Db	302	CAACAACAGTTGAAGACACTCATACGGGAGAGAAACACAACTTGAGCGATTGAATGTG	361
		: : : :	
Qy	107	GluGluGlnSerLeuIleLysValLysGlyGluGlnLeuMetIleGlnLysLeuSer	126
		:	
Db	362	CAACACCAAGTCTCAAGAAAACAGAGCGCTGACAGAGTTCAATTGACCAATTCCTCA	421
		:	
Qy	127	AspSer	128
Db	422	ACTTCT	427

RESULT 5	
BP026060	
LOCUS	540 bp mRNA linear EST 15-MAR-2002
DEFINITION	BP026060 K. Inaba unpublished cDNA library, testis Ciona intestinalis cDNA clone cits42a19 5', mRNA sequence.
ACCESSION	BP026060
VERSION	BP026060.1
KEYWORDS	GI:19518010
SOURCE	EST.
ORGANISM	Ciona intestinalis Ciona intestinalis Ciona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.
REFERENCE	1 (bases 1 to 540)
AUTHORS	Inaba,K., Padma,P., Satouh,Y., Shin-i.T., Kohara,Y., Satoh,N. and Satou,Y.
TITLE	EST analysis of gene expression in testis of the ascidian Ciona intestinalis
JOURNAL	Mol. Reprod. Dev., (2002) In press
COMMENT	Contact: Kazuo Inaba Asamushi Marine Biological Statio Tohoku University Asamushi, Aomori, Aomori 039-3501, Japan Tel: 81-17-752-3394 Fax: 81-17-752-2765 Email: inaba@biology.tohoku.ac.jp.

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FEATURES
  source      1..540
              Location/Qualifiers
                email: inabaepidology.tonoku.ac.jp.
                /organism="Ciona intestinalis"
                /mol_type="mRNA"
                /db_xref="taxon:7719"
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BASE COUNT
ORIGIN
189 a 101 c 102 g 147 t
/cclone="cits42a19"
/tissue_type="testis"
/cclone_lib="K. Inaba unpublished cDNA library, testis"
1 others

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Alignment Scores:	4.01e-08	Length:	540
Pred. No.:	200.00	Matches:	41
Score:	61.48%	Conservative:	34
Percent Similarity:	33.61%	Mismatches:	47
Best Local Similarity:	30.26%	Indels:	0
Query Match:	12	Gaps:	0
DB:	12		

US-09-866-582A-2 (1-135) x BP026060 (1-540)

Qy	7	GlyValTyrpheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla	26
Db	83	GGGCTTCATTGTGACGAAGTTAAACAAGGTCAGAGCTTTTAAAAACGACACACTAATCAGCAG	142
Qy	27	SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly	46
Db	143	ACATCTGAACCTGAAAGAGGAATGCCAGCAATTCCTCTCGAAAAATCGACCACTTTCCAAAAA	202
Qy	47	LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys	66
Db	203	CTTGCTGGTAGCTCATAGAAATGACCGACCCATCGCAAAAGATGTTGAAAATGAGAAA	262
Qy	67	LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys	86
Db	263	ATGAAGCCCATCGGTTCTCGTAACTAGTCAAGTCAATTGCCAAGCAGAGGAAATCCACG	322
Qy	87	GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuArgLeuGlnMet	106
Db	323	CAACAACAGTGTGAAGCAGCACTATACGCGGAGAGAAGAAACACAACTTGACCGATTGAATGTG	382
Qy	107	GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer	126
Db	383	CAACACAGTCTCTGAGGAAACAAGAGGCCGCAACAAGTTGAATTCATTGACCAATTCCTCA	442
Qy	127	AspSer	128
Db	443	ACTTCT	448

RESULT 6
AV964246
LOCUS
DEFINITION
AV964246
541 bp mRNA linear EST 14-MAR-2000
AV964246 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone cieg17g02 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 541)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

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FEATURES
source
1. 541
Location/Qualifiers
/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg17a02"

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/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

BASE COUNT   188 a   97 c   103 g   153 t
ORIGIN

Alignment Scores:
Pred. No.:      4.02e-08      Length:      541
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:               9      Gaps:      0

US-09-866-582A-2 (1-135) x AV964246 (1-541)

QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 69 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTTTAAACACGACAGCACTAATCAGCAG 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 129 ACATCTGAACGAAAGAGGAATGCCGAATTCGCTCGAAATCGCAGACAGTTCCTCAAAA 188
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 189 CTGTGTGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 248
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 249 ATGAAGGCATCGGTTCGTAACATGCTCAAGTCAATTCGCAAGAGGAGGAAATCCCGAG 308
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGlnGluGluArgLeuGlnMet 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 309 CAACACAGCTGTAAGAGCACTCATAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 107 GluGluGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 369 CAACACCAAGTCTCTGAGGAAACAAGAGGCGGCAACAAGTGAATTCATTGACCAATCTCA 428
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 AspSer 128
   |||
D6 429 ACTTCT 434

RESULT 7
BW215694
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 565)
AUTHORS
Satoh,Y., Shin-I.T., Kohara,Y. and Satoh,N.
TITLE
Expressed genes in Ciona intestinalis (2002c)
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scid.ian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..565
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg080k13"

FEATURES
source
1..565
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg080k13"

/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

BASE COUNT   195 a   99 c   109 g   162 t
ORIGIN

Alignment Scores:
Pred. No.:      4.16e-08      Length:      565
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:               13      Gaps:      0

US-09-866-582A-2 (1-135) x BW215694 (1-565)

QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 71 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTTTAAACACGACAGCACTAATCAGCAG 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 131 ACATCTGAACGAAAGAGGAATGCCGAATTCGCTCGAAATCGCAGACAGTTCCTCAAAA 190
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 191 CTGTGTGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 250
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 251 ATGAAGGCATCGGTTCGTAACATGCTCAAGTCAATTCGCAAGAGGAGGAAATCCCGAG 310
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGlnGluGluArgLeuGlnMet 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 311 CAACACAGCTGTAAGAGCACTCATAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 107 GluGluGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 371 CAACACCAAGTCTCTGAGGAAACAAGAGGCGGCAACAAGTGAATTCATTGACCAATCTCA 430
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 AspSer 128
   |||
D6 431 ACTTCT 436

RESULT 8
BP013658
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 576)
AUTHORS
Satoh,N., Satou,Y., Kohara,Y. and Shin-I.T.
TITLE
Expressed genes in Ciona intestinalis
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scid.ian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..576
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad57n03"

FEATURES
source
1..576
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad57n03"
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/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
BASE COUNT      201 a   99 c   109 g   166 t   1 others
ORIGIN

Alignment Scores:
Pred. No.:      4.23e-08      Length:      576
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:      30.26%      Indels:      0
DB:              12          Gaps:         0

US-09-866-582A-2 (1-135) x BP013658 (1-576)

QY  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  52 GGCCTTCATTTGACCAAGTTTACAAGCTCAGAGTTTAAACCCAGACACATAATCAGCAG 111
QY  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 ACATCTGAACCTGAAGAGGAATGCCACGAATTCGTCTCGAANAATCACCAGTTTCAAAA 171
QY  47 LeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAlaGluLys 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 CTGTGTGGTAGCTTCATAGAAATGACCGACACAAATCGCAAAAGATGTTGAAATGAGAAA 231
QY  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 ATGAAGCCATCGGTCTCGTACATGCTCAAGTCAATTCGCAAGCAGAGGAATCCCGAG 291
QY  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGluMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  292 CAACACACAGTTGAAAGCACTCATAGCGGAGAGAGAAAACACAACTTGAGCGATTGAATGTG 351
QY  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  352 CAACACCACTCTCTGAGGAACAAGAGCCGCAACAAGTTGAATTGATTCATTCACCAATTCCTCA 411
QY  127 AspSer 128
    |||
Db  412 ACTTCT 417

RESULT 9
BP008971
LOCUS
DEFINITION
BP008971 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad50e21 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 670)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
Expressed genes in Ciona intestinalis
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .670
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"

FEATURES
source

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/clone="ciad50e21"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
BASE COUNT      234 a   108 c   118 g   209 t   1 others
ORIGIN

Alignment Scores:
Pred. No.:      4.78e-08      Length:      670
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:      30.26%      Indels:      0
DB:              12          Gaps:         0

US-09-866-582A-2 (1-135) x BP008971 (1-670)

QY  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  67 GGCCTTCATTTGACCAAGTTTACAAGCTCAGAGTTTAAACCCAGACACATAATCAGCAG 126
QY  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  127 ACATCTGAACCTGAAGAGGAATGCCACGAATTCGTCTCGAANAATCACCAGTTTCAAAA 186
QY  47 LeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAlaGluLys 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  187 CTGTGTGGTAGCTTCATAGAAATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 246
QY  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  247 ATGAAGCCATCGGTCTCGTACATGCTCAAGTCAATTCGCAAGCAGAGGAATCCCGAG 306
QY  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGluMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  307 CAACACACAGTTGAAAGCACTCATAGCGGAGAGAGAAAACACAACTTGAGCGATTGAATGTG 366
QY  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  367 CAACACCACTCTCTGAGGAACAAGAGCCGCAACAAGTTGAATTGATTCATTCACCAATTCCTCA 426
QY  127 AspSer 128
    |||
Db  427 ACTTCT 432

RESULT 10
BP008971
LOCUS
DEFINITION
BP008971 Nori Satoh unpublished cDNA library, neural complex Ciona
intestinalis cDNA clone ciad50e21 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 680)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .680
/organism="Ciona intestinalis"
/mol_type="mRNA"

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/db_xref="taxon:7719"
 /clone="cinc003m02"
 /tissue_type="neural complex"
 /clone_lib="Nori Satoh unpublished cDNA library, neural complex"

BASE COUNT 245 a 107 c 120 g 208 t

ORIGIN

Alignment Scores:
 Pred. No.: 4.84e-08 Length: 680
 Score: 200.00 Matches: 41
 Percent Similarity: 61.48% Conservatives: 47
 Best Local Similarity: 33.61% Mismatches: 34
 Query Match: 30.26% Indels: 0
 DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW298785 (1-680)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
 |||:|||||:|||||: |||
 Db 52 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTGTAAACACGACACTAATCAGCAG 111
 Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
 |||:|||||:|||||: |||
 Db 112 ACATCTGAACCTGAAGAGGAATGCCAGCAATTCGTCTCGAAATCGACCACTTTCAAAA 171
 Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
 |||:|||||:|||||: |||
 Db 172 CTTGTTGGTAGCTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 231
 Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
 |||:|||||:|||||: |||
 Db 232 ATGAAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGCCAAGCAGAGGGAATCCAG 291
 Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
 |||:|||||:|||||: |||
 Db 292 CAACAACAGTTGAAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGGATTCGAATGTG 351
 Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
 |||:|||||:|||||: |||
 Db 352 CAACACAGTCTCTAAGAAACACAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 411
 Qy 127 AspSer 128
 |||
 Db 412 ACTTCT 417

RESULT 11
 BW313621 683 bp mRNA linear EST 11-NOV-2002
 LOCUS
 DEFINITION BW313621 Nori Satoh unpublished cDNA library, heart Ciona
 intestinalis cDNA clone ciht026p02 5', mRNA sequence.
 ACCESSION BW313621
 VERSION BW313621.1 GI:24894232
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 683)
 Satou, I., Shin-I, T., Kohara, Y. and Satoh, N.
 TITLE Expressed genes in Ciona intestinalis (2002c)
 JOURNAL Unpublished
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 1..683
 /organism="Ciona intestinalis"
 /mol_type="mRNA"

/db_xref="taxon:7719"
 /clone="ciht026p02"
 /tissue_type="heart"
 /clone_lib="Nori Satoh unpublished cDNA library, heart"

BASE COUNT 242 a 108 c 123 g 210 t

ORIGIN

Alignment Scores:
 Pred. No.: 4.86e-08 Length: 683
 Score: 200.00 Matches: 41
 Percent Similarity: 61.48% Conservatives: 34
 Best Local Similarity: 33.61% Mismatches: 47
 Query Match: 30.26% Indels: 0
 DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW313621 (1-683)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
 |||:|||||:|||||: |||
 Db 63 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTGTAAACACGACACTAATCAGCAG 122
 Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
 |||:|||||:|||||: |||
 Db 123 ACATCTGAACCTGAAGAGGAATGCCAGCAATTCGTCTCGAAATCGACCACTTTCAAAA 182
 Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
 |||:|||||:|||||: |||
 Db 183 CTTGTTGGTAGCTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 242
 Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
 |||:|||||:|||||: |||
 Db 243 ATGAAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGCCAAGCAGAGGGAATCCAG 302
 Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
 |||:|||||:|||||: |||
 Db 303 CAACAACAGTTGAAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGGATTCGAATGTG 362
 Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
 |||:|||||:|||||: |||
 Db 363 CAACACAGTCTCTAAGAAACACAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 422
 Qy 127 AspSer 128
 |||
 Db 423 ACTTCT 428

RESULT 12
 BW079944 715 bp mRNA linear EST 20-OCT-2002
 LOCUS
 DEFINITION BW079944 Nori Satoh unpublished cDNA library, egg Ciona
 intestinalis cDNA clone rcieg080k13 3', mRNA sequence.
 ACCESSION BW079944
 VERSION BW079944.1 GI:24181356
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 715)
 Satou, I., Shin-I, T., Kohara, Y. and Satoh, N.
 TITLE Expressed genes in Ciona intestinalis (2002c)
 JOURNAL Unpublished
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 1..715
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"

```

/clone="rcieg080k13"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT      225 a 123 c 115 g 252 t
ORIGIN

Alignment Scores:
Pred. No.:      5.04e-08      Length:      715
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13      Gaps:      0

US-09-866-582A-2 (1-135) x BW079944 (1-715)
Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAla 26
Db 669 GGGCTTCATTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 610
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 609 ACATCTGAACCTGAAGAGGAATGCCACGAATTCCTCGAAATCGACACAGTTTCAAAAA 550
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 549 CTTGTTGTTAGCTTCATAGAATGACCGCACACATCGCAAAAGATGTTGAAATGAGAAA 490
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 489 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTTGCAAGCAGAGGGAATCCCG 430
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
Db 429 CAACAACAGTGTGAAAGCACTCATACGGGAGGAAGAAACACAACTGAGCGATTGAATGTG 370
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 369 CAACACCAAGTCTCTGAGGAACAAGAGGCCGCAACAAGTTGAATTCATTGACCAATTCTCA 310
Qy 127 AspSer 128
Db 309 ACTTCT 304

RESULT 13
BW168960/c
LOCUS
DEFINITION
intestinalis cDNA clone rcieg080k13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 719)
AUTHORS
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE
Expressed genes in Ciona intestinalis (2002c)
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .719
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
FEATURES
source

/clone="rcinc003m02"
/tissue_type="neural complex"
/clone_lib="Nori Satoh unpublished cDNA library, neural complex"
BASE COUNT      226 a 124 c 110 g 259 t
ORIGIN

Alignment Scores:
Pred. No.:      5.06e-08      Length:      719
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13      Gaps:      0

US-09-866-582A-2 (1-135) x BW168960 (1-719)
Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAla 26
Db 668 GGGCTTCATTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 609
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 608 ACATCTGAACCTGAAGAGGAATGCCACGAATTCCTCGAAATCGACACAGTTTCAAAAA 549
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 548 CTTGTTGTTAGCTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 489
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 488 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTTGCAAGCAGAGGGAATCCCG 429
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
Db 428 CAACAACAGTGTGAAAGCACTCATACGGGAGGAAGAAACACAACTGAGCGATTGAATGTG 369
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 368 CAACACCAAGTCTCTAAGAAACAAGAGCGTGAACAGTTGAATTCATTGACCAATTCTCA 309
Qy 127 AspSer 128
Db 308 ACTTCT 303

RESULT 14
BW077451/c
LOCUS
DEFINITION
intestinalis cDNA clone rcieg072121 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE
1 (bases 1 to 720)
AUTHORS
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE
Expressed genes in Ciona intestinalis (2002c)
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .720
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
FEATURES
source

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```

/clone="cieg072121"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

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```

BASE COUNT      224 a 124 c 112 g 260 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5.07e-08      Length:      720
Score:          200.00      Matches:    41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:    30.26%      Indels:    0
DB:            13          Gaps:      0

```

US-09-866-582A-2 (1-135) x BW077451 (1-720)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  656 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 597

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  596 ACATCTGAAGTGAAGAGGATGCCAGCAATTCGTCTCGAAATCGACCAGTTTCAAAA 537

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  536 CTTGTTGAGTTCATAGAAATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 477

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  476 ATGAAGCCATCGGTTCTCTAAGTCAATTCGCAAGAGGAGGAGGATCCAG 417

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  416 CAACAACAGTTGAAGCACTCATAGCGGAGAGAGAAACACAACTTGAGCGATTGAATGTG 357

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGlnGluLeuMetIleGlnLysLeuSer 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  356 CAACACCAAGTCTCTGAGGAAACAAGAGCGCGCAACAAGTTGAATTCATTGACCAATTCTCA 297

Qy  127 AspSer 128
    |||
Db  296 ACTTCT 291

```

```

RESULT 15
BW213159
LOCUS      BW213159      755 bp      mRNA      linear      EST 05-NOV-2002
DEFINITION      BW213159 Nori Satoh unpublished cDNA library, egg Ciona
                 intestinalis cDNA clone cie072121 5', mRNA sequence.
ACCESSION      BW213159
VERSION        BW213159.1 GI:24627773
KEYWORDS      EST.
SOURCE        Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 755)
AUTHORS      Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE        Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
FEATURES             source
                    1..755
                    /organism="Ciona intestinalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:7719"

```

```

/clone="cieg072121"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

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```

BASE COUNT      267 a 117 c 130 g 241 t
ORIGIN

```

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Alignment Scores:
Pred. No.:      5.27e-08      Length:      755
Score:          200.00      Matches:    41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:    30.26%      Indels:    0
DB:            13          Gaps:      0

```

US-09-866-582A-2 (1-135) x BW213159 (1-755)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  76 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 135

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  136 ACATCTGAAGTGAAGAGGATGCCAGCAATTCGTCTCGAAATCGACCAGTTTCAAAA 195

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  196 CTTGTTGAGTTCATAGAAATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 255

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  256 ATGAAGCCATCGGTTCTCTAAGTCAATTCGCAAGAGGAGGAGGATCCAG 315

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  316 CAACAACAGTTGAAGCACTCATAGCGGAGAGAGAAACACAACTTGAGCGATTGAATGTG 375

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGlnGluLeuMetIleGlnLysLeuSer 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  376 CAACACCAAGTCTCTGAGGAAACAAGAGCGCGCAACAAGTTGAATTCATTGACCAATTCTCA 435

Qy  127 AspSer 128
    |||
Db  436 ACTTCT 441

```

```

RESULT 16
AV897763/c
LOCUS      AV897763      758 bp      mRNA      linear      EST 09-NOV-2001
DEFINITION      AV897763 Nori Satoh unpublished cDNA library, young adult Ciona
                 intestinalis cDNA clone rciad50e21 3', mRNA sequence.
ACCESSION      AV897763
VERSION        AV897763.1 GI:16886861
KEYWORDS      EST.
SOURCE        Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 758)
AUTHORS      Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
TITLE        Expressed genes in Ciona intestinalis
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
FEATURES             source
                    1..758
                    /organism="Ciona intestinalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:7719"

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/db_clone="rciad50e21"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
BASE COUNT      241 a 131 c 119 g 267 t
ORIGIN

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Alignment Scores:
Pred. No.:      5,29e-08      Length:      758
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:    30.26%      Indels:      0
DB:              9          Gaps:      0

```

US-09-866-582A-2 (1-135) x AV897763 (1-758)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  679 GGGCTTCATTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 620
Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  619 ACATCTGAACCTGAAGAAGAAATGCCAGCAATTCGTCTCGAAATATCGACCAAGTTTCAAAA 560
Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  559 CTTGTTGTAGCTTCATAGAATGACCGCCCAATCCGAAAGATGTTGAAATGAGAAA 500
Qy  67 LeuTysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  499 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGTCGAAGAGGAGGAAATCCAG 440
Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGluMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  439 CAACAACAGTTGAAGCACTCATAGCGGAGAAGAAACACAACTTGAGCGATTGAATGTG 380
Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  379 CAACACCAAGTCTCTGAGGAACAAGAGCGCGCAACAAGTTGAATTCATTGACCAATTCCTCA 320
Qy  127 AspSer 128
|||
Db  319 ACTTCT 314

```

```

RESULT 17
BW312507
LOCUS      BW312507      759 bp      mRNA      linear      EST 11-NOV-2002
DEFINITION      intestinalis cDNA clone ciht023e11 5', mRNA sequence.
ACCESSION      BW312507
VERSION        BW312507.1      GI:24893118
KEYWORDS
SOURCE
ORGANISM      Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Clonidae; Ciona.
REFERENCE      1      (bases 1 to 759)
AUTHORS      Satou,Y., Shin-I.T., Kohata,Y. and Satoh,N.
TITLE        Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@cscidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
                1..759
                  /organism="Ciona intestinalis"
                  /mol_type="mRNA"

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```

FEATURES
source

```

```

/db_xref="taxon:7719"
/clone="ciht023e11"
/tissue_type="heart"
/clone_lib="Nori Satoh unpublished cDNA library, heart"
BASE COUNT      275 a 113 c 133 g 238 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5,29e-08      Length:      759
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:    30.26%      Indels:      0
DB:              13         Gaps:      0

```

US-09-866-582A-2 (1-135) x BW312507 (1-759)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  54 GGGCTTCATTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 113
Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  114 ACATCTGAACCTGAAGAAGAAATGCCAGCAATTCGTCTCGAAATATCGACCAAGTTTCAAAA 173
Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  174 CTTGTTGTAGCTTCATAGAATGACCGCCCAATCCGAAAGATGTTGAAATGAGAAA 233
Qy  67 LeuTysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  234 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGTCGAAGAGGAGGAAATCCAG 293
Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGluMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  294 CAACAACAGTTGAAGCACTCATAGCGGAGAAGAAACACAACTTGAGCGATTGAATGTG 353
Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  354 CAACACCAAGTCTCTAAGAAAACAAGAGCGCTCAAGTGAATTCATTGACCAATTCCTCA 413
Qy  127 AspSer 128
|||
Db  414 ACTTCT 419

```

```

RESULT 18
BW393735
LOCUS      BW393735      615 bp      mRNA      linear      EST 22-MAY-2002
DEFINITION      NISC_ng05b11.y1.NICHD_XGC_Emb6 Silurana tropicalis cDNA clone
IMAGE:5382476 5', mRNA sequence.
ACCESSION      BQ393735
VERSION        BQ393735.1      GI:21081422
KEYWORDS
SOURCE
ORGANISM      Silurana tropicalis (western clawed frog)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
              Xenopodinae; Silurana.
REFERENCE      1      (bases 1 to 615)
AUTHORS      NTH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.
TITLE        National Institute of Child Health and Human Development, National
              Cancer Institute, Xenopus Gene Collection
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              CDNA Library Preparation:
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
              DNA Sequencing by: National Institutes of Health Intramural
              Sequencing Center (NISC)
              Clone distribution: NCI-CCAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              info@image.llnl.gov
              Plate: LLAM11974      row: C      column: 21

```


[illegible]

Qy 125 Leuser 126

Db 411 TTTAAC 416

RESULT 22
BY6351126

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY6351126 418 bp mRNA linear EST 15-DEC-2002
 cDNA clone K430066M20 3', mRNA sequence.
 BY6351126
 BY6351126.1 GI:26970308
 EST.

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 418)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
 Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
 Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,
 Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
 Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani,
 L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest,
 A., Fraser, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
 Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,
 Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,
 King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
 P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Mikl,
 H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,
 Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
 Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,
 B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,
 M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
 R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
 Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa,
 M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
 Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,
 M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
 Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
 K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
 E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

22354683
 12468851

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 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,
 T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,
 Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
 Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,
 M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
 Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Hensch (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

Location/Qualifiers

1..418

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="K430066M20"

/tissue_type="visual cortex"

/clone_lib="RIKEN full-length enriched, visual cortex"

BASE COUNT 134 a 70 c 120 g 94 t

ORIGIN

Alignment Scores:

Pred. No.: 5.36e-08 Length: 418

Score: 197.50 Matches: 41

Percent Similarity: 61.83% Conservativeness: 40

Best Local Similarity: 31.30% Mismatches: 45

Query Match: 29.88% Indels: 5

DB: 13 Gaps: 1

US-09-866-582A-2 (1-135) x BY6351126 (1-418)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgLeuLeuAspValAspLysTyr 24

Db 10 GAGGCGAGGGTGGTCAATTTTGTATGAACCTCAAGCAAGCTCGAGTGTGGACCCAGAGGTCAACC 69

Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheLeuAsnAsnLeuGlnAsnMet 44

Db 70 CACGAGACTGTGAGCTCAAGGAGGAGTCAAGGAGTGTGGTGGCAAAATTTGGCCAGTTT 129

Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64

Db 130 CAGAAAATTTCTGGTGGTCTTAATTTGAGCTTGTTCATCAGCTTGCCAAAAGAGCAGAGAAC 189

Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84

Db 190 GAGAAGATGAAGCCATTGTGTCGGAACCTTGTGAAGTCCATAGCCAAAGCAGAGAGAA 249

Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104

Db 250 GCCCAGCAGCAGCAGCTGCGAGGCCCTATGACAGAAAAGAGAGCAGCAGTAGAAGGTAT 309

Qy 105 GlnMetGluGluGlnSerLeuLysValLysGlyGluGln-----Glu 119

Db 310 CGGTTGAATTAAGCTTTCTGTAAGTAGAAGCAGACCAACAAATGAATTTATTGACCAA 369

Qy 120 LeuMetGlnLysLeuSerAspSerSer 130

Db 370 TTTATTTTTCAGAAATGAACCTGAAATTTTCAGT 402

RESULT 23

BW150890/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

715 bp mRNA linear EST 03-NOV-2002

BW150890 Nori Satoh unpublished cDNA library, gonad Ciona

intestinalis cDNA clone rcig4013n23 3', mRNA sequence.

BW150890

BW150890.1 GI:24508115

EST.

Ciona intestinalis

Ciona intestinalis

REFERENCE 1 (bases 1 to 661)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. .661
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"
/clone="rciad74m19"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
BASE COUNT 204 a 110 c 106 g 238 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 1.05e-07 Length: 661
Score: 196.00 Matches: 40
Percent Similarity: 61.16% Conservative: 34
Best Local Similarity: 33.06% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 9 Gaps: 0

US-09-866-582A-2 (1-135) x AV899426 (1-661)

Qy 8 ValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAlaSer 27
Db 659 CTTTCATTTTGAGGAAGTTCAGCAATTCGCTCGAAATCGACCAGTTCACAAACTT 600
Qy 28 LysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGlyLeu 47
Db 599 TCTGAACCTGAAGAGGAATGCCAGCAATTCGCTCGAAATCGACCAGTTCACAAACTT 540
Qy 48 ValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLysLeu 67
Db 539 GTTGGTAGCTTCATAGAAATGACCGAGCAATCGCAAAAGATGTTGAAATGAGAAATG 480
Qy 68 LysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLysGln 87
Db 479 AAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAGCAA 420
Qy 88 LysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMetGlu 107
Db 419 CAACAGTTGAAGCACTCATAGCGAGAGAGAAACACAACTTGAGCGATTGAATGTCAA 360
Qy 108 GluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSerAsp 127
Db 359 CACCACTCTCTGAGGAACAAGAGCGCGCAACAAGTTGAATTCATTGACCAATTCCTCACT 300
Qy 128 Ser 128
Db 299 TCT 297

RESULT 26
BW248613
LOCUS BW248613 674 bp mRNA linear EST 09-NOV-2002
DEFINITION BW248613 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb078f08 5', mRNA sequence.
ACCESSION BW248613
VERSION BW248613.1 GI:24828531
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 674)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. .674
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"
/clone="citb078f08"
/tissue_type="whole animal"
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/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"
BASE COUNT 238 a 107 c 119 g 210 t
ORIGIN

Alignment Scores:
Pred. No.: 1.06e-07 Length: 674
Score: 196.00 Matches: 40
Percent Similarity: 61.48% Conservative: 35
Best Local Similarity: 32.79% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW248613 (1-674)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAla 26
Db 65 GGGCTTCATTTTGAGGAAGTTAAACAAGCTCAGAGTCTTAAACACAGAGCACTAATCAGCAG 124
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 125 ACATCTGAACGAAAGAGGAATGCCAGCAATTCGTCGCAAAATCGACCAGTTTCAAAA 184
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 185 CTTGTGTGAGCTTCATAGAAATGACCGCAATCGCAAAAGATGTTGAAATGAGAA 244
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 245 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAG 304
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
Db 305 CAACACAGTTGAAAGCACTCATAGCGAGAGAGAAACACAACTTGAGCGATTGAATGTG 364
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 365 CAACACAGTCTCTTAAGAAACAAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 424
Qy 127 AspSer 128
Db 425 ACTTCT 430

RESULT 27
BW156639/c
LOCUS BW156639 718 bp mRNA linear EST 03-NOV-2002
DEFINITION BW156639 Nori Satoh unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcigd002d11 3', mRNA sequence.
ACCESSION BW156639
VERSION BW156639.1 GI:24513864
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 718)
AUTHORS Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.
TITLE Expressed genes in *Ciona intestinalis* (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source 1..718
/organism="Ciona intestinalis"
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/db_xref="taxon:7719"
/clone="rcig002d11"
/tissue_type="gonad"
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ORIGIN

Alignment Scores:
Pred. No.: 1.12e-07 Length: 718
Score: 196.00 Matches: 40
Percent Similarity: 61.48% Conservative: 35
Best Local Similarity: 32.79% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW156639 (1-718)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db 670 GGGCTTCAATTTGACGAAGTTAAACAGCTCAGAGCTTTAAACAGAGACTAATCAGCAG 611
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 610 ACATCTGAACCTGAAAGAGGAATGCCACGAATCTGCTCGAAATCGACCACTTTCAAAA 551
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 550 CTTGTTGTAGCTTCATAGAATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 491
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 490 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATGTCACAGCAGAGGGAATCCAG 431
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
Db 430 CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAACACAACTTGAGCGATTGAATGTG 371
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 370 CAACACCACTCTCTAAGAAAACAGAGGCTGAACAAAGTTGAATTCATTGACCAATTCCTCA 311
Qy 127 AspSer 128
Db 310 ACTTCT 305

RESULT 28
BW117926/c 742 bp mRNA linear EST 24-OCT-2002
LOCUS BW117926 Nori Satoh unpublished cDNA library, tailbud embryo *Ciona*
DEFINITION *intestinalis* cDNA clone rcitb078f08 3', mRNA sequence.
ACCESSION BW117926
VERSION BW117926.1 GI:24364591
KEYWORDS EST.
SOURCE *Ciona intestinalis*
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 742)
AUTHORS Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.
TITLE Expressed genes in *Ciona intestinalis* (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source 1..742
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcitb078f08"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

BASE COUNT 233 a 130 c 114 g 265 t
ORIGIN

Alignment Scores:
Pred. No.: 1.15e-07 Length: 742
Score: 196.00 Matches: 40
Percent Similarity: 61.48% Conservative: 35
Best Local Similarity: 32.79% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW117926 (1-742)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db 668 GGGCTTCAATTTGACGAAGTTAAACAGCTCAGAGCTTTAAACAGAGACTAATCAGCAG 609
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 608 ACATCTGAACCTGAAAGAGGAATGCCACGAATCTGCTCGAAATCGACCACTTTCAAAA 549
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 548 CTTGTTGTAGCTTCATAGAATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 489
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 488 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATGTCACAGCAGAGGGAATCCAG 429
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
Db 428 CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAACACAACTTGAGCGATTGAATGTG 369
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 368 CAACACCACTCTCTAAGAAAACAGAGGCTGAACAAAGTTGAATTCATTGACCAATTCCTCA 309
Qy 127 AspSer 128
Db 308 ACTTCT 303

RESULT 29
BJ064012 548 bp mRNA linear EST 07-DEC-2001
LOCUS BJ064012 NIBB Mochii normalized Xenopus tailbud library
DEFINITION *laevis* cDNA clone XL078b07 5', mRNA sequence.
ACCESSION BJ064012
VERSION BJ064012.1 GI:17424850
KEYWORDS EST.
SOURCE *Xenopus laevis* (African clawed frog)
ORGANISM *Xenopus laevis*


```

Db      88  GAGCGGGTTCAGCTTGTATGAGCTGAACAAATTCGTATCTTGACCCCGACGCTCC 147
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Qy      25  AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
      ::  |||:||||:||||:|||||  |||  |||
Db      148  CAGCAAAACACCAACCAATTAAGAGGAGAGTCCGAGATTTTGTAGACAAATAGGACATTTT 207
      |||  |||:||||:||||:|||||  |||  |||
Qy      45  GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
      |||  |||:||||:||||:|||||  |||  |||
Db      208  CAGAAAGTAGTGGGTGGACTAATTGAGCTTTGTATGAGTGTAGCTTAAGAAACCCGAAAC 267
      |||  |||:||||:||||:|||||  |||  |||
Qy      65  GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
      |||  |||:||||:||||:|||||  |||  |||
Db      268  GAGAAATGAAGCAATAGTGCCTGCGGAACTTGTCTTAAATCTATAGCAAGCAGAGAGAA 327
      |||  |||:||||:||||:|||||  |||  |||
Qy      85  ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
      |||  |||:||||:||||:|||||  |||  |||
Db      328  GCCCAGCAGCAGCACTATATGCTTAAAGTGAAGCTGAGCAAAATGAATGAGAAAGGTAC 387
      |||  |||:||||:||||:|||||  |||  |||
Qy      105  GlnMetGluGlnGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGlnLys 124
      |||  |||:||||:||||:|||||  |||  |||
Db      388  CGAATAGATACGACGCTCTGTCTAAAGTGAAGCTGAGCAAAATGAATTTATTGATCAA 447
      |||  |||:||||:||||:|||||  |||  |||
Qy      125  LeuSer 126
      ::
Db      448  TTTAAAC 453

RESULT 31
BE884392 601505670F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907361 5',
LOCUS mRNA sequence.
DEFINITION BE884392
VERSION BE884392.1 GI:103333168
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9717 row: 1 column: 18
High quality sequence stop: 642.
FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:3907361"
        /tissue_type="leptomysarcoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_71"
        /note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: NotI;
        Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 2.1 kb."
BASE COUNT 274 a 203 c 244 g 196 t
ORIGIN
Alignment Scores: 1.66e-07 Length: 917
Pred. No.: 195.00 Matches: 39
Score: 62.81% Conservative: 37
Percent Similarity:

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Best Local Similarity: 32.23% Mismatches: 45
Query Match: 29.50% Indels: 0
DB: 10 Gaps: 0

US-09-866-582a-2 (1-135) x BE884392 (1-917)

Qy      4  ValAspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLys 23
      |||  |||:||||:||||:|||||  |||  |||
Db      105  GTGAGCAGGGCTACACTTTTCATGACTGAACAAGCTGAGGCTGTGGACCCAGAGGTT 164
      |||  |||:||||:||||:|||||  |||  |||
Qy      24  TyrAsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsn 43
      ::  |||:||||:||||:|||||  |||  |||
Db      165  ACCCAGCAGCATAGCTGAGCTGAAGGAAGAGTGTCAAGAGACTTTGTGGACAAATTTGGCCAG 224
      |||  |||:||||:||||:|||||  |||  |||
Qy      44  MetGlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGlu 63
      |||  |||:||||:||||:|||||  |||  |||
Db      225  TTTCAAAATAGTGTGGTGTATTAATGAGCTTTGTGATCAACTTCCAAAGAACAGAGAA 284
      |||  |||:||||:||||:|||||  |||  |||
Qy      64  AlaGluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArg 83
      |||  |||:||||:||||:|||||  |||  |||
Db      285  AATGAAAGATGAAGCCATCGTCTCGGAACTTGTCTCAATCTATAGCAAGCAGAGA 344
      |||  |||:||||:||||:|||||  |||  |||
Qy      84  LysArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArg 103
      |||  |||:||||:||||:|||||  |||  |||
Db      345  GAAGCTCAACAGCAGCACTTCAAGCCCTAATAGCAGAAAGAAATGTCAGCTAGAAAG 404
      |||  |||:||||:||||:|||||  |||  |||
Qy      104  LeuGlnMetGluGlnGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGln 123
      |||  |||:||||:||||:|||||  |||  |||
Db      405  TATCGGGTTGAATATCAAGCTTTGTGTAAGTAGAAGCAGACAAATGAATTTATTGAC 464
      |||  |||:||||:||||:|||||  |||  |||
Qy      124  Lys 124
      ::
Db      465  CAA 467

RESULT 32
AI703692 427 bp mRNA linear EST 03-JUN-1999
LOCUS UI-R-ABI-yu-h-06-0-UI.s1 UI-R-ABI Rattus norvegicus cDNA clone
DEFINITION AI703692
ACCESSION AI703692
VERSION AI703692.1 GI:4991592
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 427)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT 889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
    source
    Location/Qualifiers
        1..427
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /strain="Sprague-Dawley"

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/db_xref="taxon:10116"
/clone="UI-R-AB1-yu-h-06-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AB1"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AB1
library is a normalized library constructed from 16.5 dpc
rat ventricle. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_SEQ=None found"

BASE COUNT 90 a 111 c 70 g 156 t
ORIGIN

Alignment Scores:
Pred. No.: 9.88e-08 Length: 427
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 9 Gaps: 1

US-09-866-582A-2 (1-135) x AI703692 (1-427)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 426 GAGCAGCGGCTGCACCTTCGATGAGCTGAACAAGCTTCGGGTGTGGACCCAGAGGTTACC 367
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 366 CAGCAGACCACGAGCTCAAGCAGAGCTGCAAGGACTTTGGGACAAAATTGGCCAGCTTT 307
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 306 CAGAAAATCGTGTGGTCTGATTGAGCTTGTTCATCAGCTTGCCAAAAGACAGAGAAC 247
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 246 GAGAAAATGAAGGCCATTTGGTGCAGAACTTGTGAAATCCATAGCGAGCAGAGAGAA 187
Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
Db 186 GCCCAGCAACGCAACTGCAGGCACTGATACAGAAAAGAGATGCCAGCTAGAAGGTAT 127
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 126 CGGCTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 67
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 66 TTTATTTTCAGAAATGAACCTGAAAATTTTCAGT 34

RESULT 33
BE196900/c 429 bp mRNA linear EST 26-JUN-2000
LOCUS ug64h07.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
DEFINITION IMAGE:1547197 3' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD
PROTEIN. ;, mRNA sequence.

ACCESSION BE196900
VERSION BE196900.1 GI:8709069
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 429)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL COMMENT

Unpublished
Other ESTs: ug64h07.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:952545.

FEATURES
source Location/Qualifiers
1. 429
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1547197"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 94 a 122 c 74 g 139 t
ORIGIN

Alignment Scores:
Pred. No.: 9.92e-08 Length: 429
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 10 Gaps: 1

US-09-866-582A-2 (1-135) x BE196900 (1-429)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 411 GAGCAGCGGCTGCACCTTCGATGAGCTGAACAAGCTTCGGGTGTGGACCCAGAGGTTACC 352
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 351 CAGCAGACTGTGGAGCTCAAGGAGGAGTGCAAGGACTTTGTGGACAAAATTGGCCAGCTTT 292
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 291 CAGAAAATTTGTGTGGTCTTAATTGAGCTTGTTCATCAGCTTGCCAAAAGACAGAGAAC 232
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 231 GAGAAAGATGAAGGCCATTTGGTTCGGAACTTGTGAACTCCATAGCCAGCAGAGAGAA 172
Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 171 GCCCAGCAGCAGCAGCTGCAGGCCCTGTAGCAGAAAAGACAGCCAGCTAGAAAGGTAT 112
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 111 CGGCTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGAACAAAATGAATTTATTGACCAA 52
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 51 TTTATTTTCAGAAATGAACCTGAAAATTTTCAGT 19

RESULT 34
BY438168
LOCUS BY438168
DEFINITION RIKEN full-length enriched, 17 days embryo kidney Mus
musculus cDNA clone I92015K14 3', mRNA sequence.
ACCESSION BY438168
VERSION BY438168.1 GI:26721595

BY438168 431 bp mRNA linear EST 13-DEC-2002
BY438168 RIKEN full-length enriched, 17 days embryo kidney Mus
musculus cDNA clone I92015K14 3', mRNA sequence.
ACCESSION BY438168
VERSION BY438168.1 GI:26721595

KEYWORDS
SOURCE
ORGANISM

EST.
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)

REFERENCE
AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani,
L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest,
A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M.,
King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons,
P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D.,
Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring,
B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou,
M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale,
R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa,
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
K., Shingagawa, A., Tsunishi, A., Yoshino, M., Waterston, R., Lander,
E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome-sc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,
T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,
M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
Location/Qualifiers
1. 431
/organism="Mus musculus"

FEATURES
source

/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1920155K14"
/tissue_type="kidney"
/dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched, 17 days embryo
kidney"
BASE COUNT 138 a 75 c 122 g 96 t
ORIGIN
Alignment Scores:
Pred. No.: 9.96e-08 Length: 431
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 20.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 13 Gaps: 1
US-09-866-582A-2 (1-135) x BY438168 (1-431)
QY 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 23 GAGCAGGGGTGTCATTTTGTATGAACCTGACCAAGCTCGCAGCTGTGGACCCAGAGGTACC 82
QY 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 83 CAGCAGACTCTGGAGCTCAAGGAGGAGCTTCTGGACAAAATGCCACGTTT 142
QY 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 143 CAGAAAATTTGGTGTGCTCAATTTAGCTTGTGATCAGCTTGCCAAAGAGCAGAGAAC 202
QY 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 203 GAGAGATGAGGCCATTTGTCGGAACCTTCTGAAGTCCATAGCAGAGCAGAGAGAA 262
QY 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLys 104
Db 263 GCCCAGCAGCAGCAGCTGCAGGCCCTCATAGCAGAAAAGAGCAGCAGCTAGAAAAGTAT 322
QY 105 GlnMetGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 323 CGGTTGAATATGAAGCTTTGTGTAAGTAGACAGACAGAAAATGAATTTATTGACCAA 382
QY 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 383 TTTATTTTTCAGAAATGAACTGAAAATTTTCACT 415
RESULT 35
AW533561/c
LOCUS
DEFINITION
UI-R-BU0-and-d-03-0-UI.s1 UI-R-BU0 Rattus norvegicus cDNA clone
UI-R-BU0-and-d-03-0-UI 3', mRNA sequence.
ACCESSION
AW533561
VERSION
AW533561.1 GI:7175975
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 432)
AUTHORS
Bonaldi, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
9704477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

[illegible]

[illegible]

COMMENT

Other_ESTs: H3085G04-5
 Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://igsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3085 row: G column: 04
 Seq primer: -21M13 Forward
 High quality sequence stop: 687
 POLYA-Yes.

FEATURES

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 /sex="Clones arrayed from a variety of cDNA libraries"
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 /lab_host="DH10B"
 /clone_lib="NIA Mouse 15K cDNA Clone Set"
 /note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
 BASE COUNT 145 a 174 c 136 g 232 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.45e-07 Length: 687
 Score: 194.50 Matches: 40
 Percent Similarity: 61.83% Conservative: 41
 Best Local Similarity: 30.53% Mismatches: 45
 Query Match: 29.43% Indels: 5
 DB: 10 Gaps: 1

US-09-866-582A-2 (1-135) x BG070290 (1-687)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
 Db 654 GAGCAGGGCTGCTATTGTATGAACTGAACAAGCTCCGAGTGTGGACCCAGAGGTCAACC 595
 Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
 Db 594 CAGCAGACTGTGGAGCTCAAGGAGCTGCAAGGACTTTGTGGACAAATTTGCCAGTTT 535
 Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
 Db 534 CAGAAATTTGTGTGTCTAATTGAGCTTGTTCATCAGCTTGCCAAAGAGCAGAGAAC 475
 Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
 Db 474 GAGAAATGAGGCCCTTGTGTGCTCGGAAGTTCGTGAAGTCCATPAGCGAGAGAGAA 415

Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
 Db 414 GCCCAGCAGCAGCAGCTGCAGGCCCTGTAGCAGAAAGAACCCAGCTAGAAAGGTAT 355
 Qy 105 GlnMetGluGluGlnSerIleLysValLysGlyGluGln-----Glu 119
 Db 354 CGGTTGAATTAAGAGCTTTGTGTAAGTAGAAGCAGACAAATAATTTATTGACCAA 295
 Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
 Db 294 TTTATTTTTCAGAAATGAACCTGAAATTTTCAGT 262

RESULT 48
 BM940927/c
 LOCUS
 DEFINITION
 UI-M-CG0p-biq-b-11-0-UI.r1.NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 UI-M-CG0p-biq-b-11-0-UI 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 691)
 Title
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: MEST@mail.nih.gov
 Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
 Medicine
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 REVERSE.
 FEATURES
 source
 1. .691
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CG0p-biq-b-11-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_Ret4_S2"
 /note="vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_Ret4_S2 library is a subtracted library,
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale
 University School of Medicine"
 BASE COUNT 158 a 185 c 148 g 199 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-07 Length: 691
 Score: 194.50 Matches: 40
 Percent Similarity: 61.83% Conservative: 41
 Best Local Similarity: 30.53% Mismatches: 45
 Query Match: 29.43% Indels: 5

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DB: 12 Caps: 1
US-09-866-582A-2 (1-135) x BM940927 (1-691)
Qy 5 AsparGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 412 GAGCAGGGCTGCAATTTTGATGAAGTCCGAGTGTGGACCCAGAGGTCAACC 353
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 352 CAGCAGACTGTGGAGCTCAGGAGGAGTCAAGGACTTTGTGGCAAAATGGCCAGTTT 293
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 292 CAGAAAATTTGTTGCTGCTTAATGAGCTTGTGATCAGCTTGCCAAAGAGCAGAGAAC 233
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 232 GAGAAGATGAAGGCCATTTGCTCGGAAGTGTCTGAAGTCCATAGCAAGCAGAGAGAA 173
Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 172 GCCCAGCAGCAGCAGCTGCGAGCCCTGATAGCAGAAAGAGAGCGCAGCTAGAAAGTAT 113
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 112 CGGCTTGAATGAAGCTTTGTGTAAGTAGAAGCAGACACAAATGAATTTATTGACCAA 53
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 52 TTTATTTTTCAGAAATGAAGTGAATAATTCAGT 20

RESULT 49
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LOCUS BQ177222 707 bp mRNA linear EST 30-APR-2002
DEFINITION UI-M-DJ2-bwa-p-16-0-UI-s1 NIH-BMAP_DJ2 Mus musculus cDNA clone
ACCESSION BQ177222
VERSION BQ177222.1 GI:20352714
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 707)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: meste@mail.nih.gov
Tissue Procurement: Dr. Robin Davison
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes
Location/Qualifiers
1..707
/organism="Mus musculus"
/mol_type="mRNA"
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/dev_stage="Adult"
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/notes=Organ: brain; Vector: pT73-Pac (Pharmacia) with a
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UI-M-DJ2 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is: GCTACATGAT, subfornical
organ and area postrema.
TAG_LIB=UI-M-DJ2
TAG_TISSUE=subfornical organ and postrema
TAG_SEQ=GCTACATGAT"
BASE COUNT 158 a 185 c 148 g 214 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 1.49e-07 Length: 707
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 13 Gaps: 1
US-09-866-582A-2 (1-135) x BQ177222 (1-707)
Qy 5 AsparGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 427 GAGCAGGGCTGCAATTTTGATGAAGTCCGAGTGTGGACCCAGAGGTCAACC 368
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 367 CAGCAGACTGTGGAGCTCAAGGAGGAGTGTGGCAAAATTTGGCCAGTTT 308
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 307 CAGAAAATTTGTTGCTGCTTAATGAGCTTGTGATCAGCTTGCCAAAGAGCAGAGAAC 248
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 247 GAGAAGATGAAGGCCATTTGCTCGGAAGTGTCTGAAGTCCATAGCAAGCAGAGAGAA 188
Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 187 GCCCAGCAGCAGCAGCTGCGAGCCCTGATAGCAGAAAGAGAGCGCAGCTAGAAAGTAT 128
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 127 CGGCTTGAATGAAGCTTTGTGTAAGTAGAAGCAGACACAAATGAATTTATTGACCAA 68
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 67 TTTATTTTTCAGAAATGAAGTGAATAATTCAGT 35
RESULT 50
BQ074519/c
LOCUS BQ074519 775 bp mRNA linear EST 13-JUN-2003
DEFINITION H3136B04-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
ACCESSION BQ074519
VERSION BQ074519.1 GI:12557088
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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